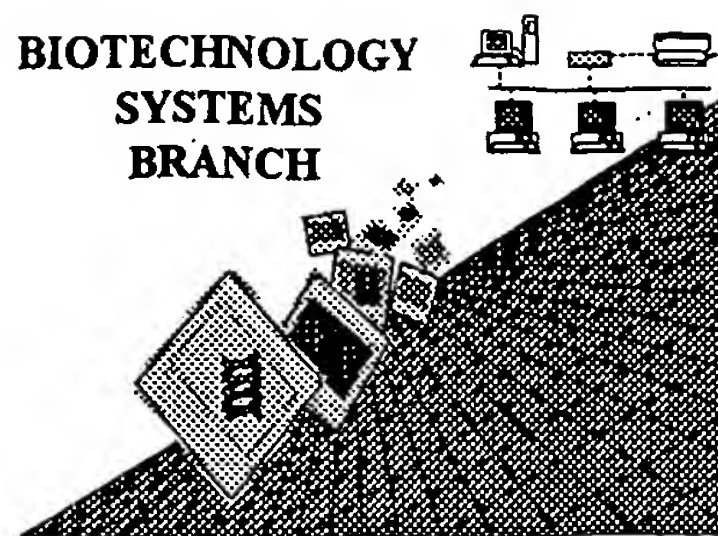BIOTECHNOLOGY
SYSTEMS
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PATENT APPLICATION: US/10/032,201   TIME: 08:06:13

Input Set : A:\351bseq.001
Output Set: N:\CRF3\01152002\J032201.raw

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  3 <110> APPLICANT: Van Rooijen, Gijs
  4          Deckers, Harm
  5          Heifetz, Peter Bernard
  6          Briggs, Steven
  7          Dalmia, Bipin Kumar
  8          Del Val, Greg
  9          Zaplachinski, Steve
 10          Moloney, Maurice
 12 <120> TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND
RELATED
 13          COMPOSITIONS
 15 <130> FILE REFERENCE: 38814-351B
 17 <140> CURRENT APPLICATION NUMBER: US/10/032,201
 18 <141> CURRENT FILING DATE: 2001-12-19
 20 <160> NUMBER OF SEQ ID NOS: 313
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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 26 <212> TYPE: DNA
 27 <213> ORGANISM: Artificial Sequence
 29 <220> FEATURE:
 30 <223> OTHER INFORMATION: Primer
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 49 <213> ORGANISM: Artificial Sequence
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 58 <211> LENGTH: 28
 59 <212> TYPE: DNA
 60 <213> ORGANISM: Artificial Sequence
 62 <220> FEATURE:
 63 <223> OTHER INFORMATION: Primer
 65 <400> SEQUENCE: 4
 66 ttaagcttca atcactctta ccttgctg                   28
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Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING   DATE: 01/15/2002
PATENT APPLICATION: US/10/032,201   TIME: 08:06:13

            Input Set : A:\35lbseq.001
            Output Set: N:\CRF3\01152002\J032201.raw

68 <210> SEQ ID NO: 5
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70 <212> TYPE: DNA
71 <213> ORGANISM: Artificial Sequence
73 <220> FEATURE:
74 <223> OTHER INFORMATION: Primer
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78 gtgatcgcct gc   72
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82 <212> TYPE: DNA
83 <213> ORGANISM: Artificial Sequence
85 <220> FEATURE:
86 <223> OTHER INFORMATION: Primer
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93 <211> LENGTH: 22
94 <212> TYPE: DNA
95 <213> ORGANISM: Artificial Sequence
97 <220> FEATURE:
98 <223> OTHER INFORMATION: Primer
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105 <212> TYPE: DNA
106 <213> ORGANISM: Artificial Sequence
108 <220> FEATURE:
109 <223> OTHER INFORMATION: Chimeric
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114 atggctaacg acatcgctcc cggtggtcaa ctaacaacca ccaccgacgt cgagaatttc 180
115 cccggatttc cagaaggtat tctcggagta gagctcactg acaaattccg taaacaatcg 240
116 gagcgattcg gtactacgat atttacagag acggtacgga aagtcgattt ctcttcgaaa 300
117 ccgtttaagc tattcacaga ttcaaaagcc attctcgctg acgctgtgat tctcgctact 360
118 ggagctgtgg ctaagcggct tagcttcgtt ggatctggtg aaggttctgg aggtttctgg 420
119 aaccgtggaa tctccgcttg tgctgtttgc gacggagctg ctccgatatt ccgtaacaaa 480
120 cctcttgcgg tgatcggtgg aggcgattca gcaatggaag aagcaaactt tcttacaaaa 540
121 tatggatcta aagtgtatat aatccatagg agagatgctt ttagagcgtc taagattatg 600
122 cagcagcgag ctttgtctaa tcctaagatt gatgtgattt ggaactcgtc tgttgtggaa 660
123 gcttatggag atggagaaag agatgtgctt ggaggattga agtgaagaa tgtggttacc 720
124 ggagatgttt ctgatttaaa agtttctgga ttgttctttg ctattggtca tgagccagct 780
125 accaagtttt tggatggtgg tgttgagtta gattcggatg gttatgttgt cacgaagcct 840
126 ggtactacac agactagcgt tcccggagtt ttcgctgcgg gtgatgttca ggataagaag 900
127 tataggcaag ccatcactgc tgcaggaact gggtgcatgg cagctttgga tgcagagcat 960

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131 <211> LENGTH: 999
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133 <213> ORGANISM: Arabidopsis thaliana
135 <400> SEQUENCE: 9
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137 cacacggcgg cgatttacgc agctagggct gaacttaaac ctcttctctt cgaaggatgg 120
138 atggctaacg acatcgctcc cggtggtcaa ctcaaccaac caccgcgtga gaatttcccc 180
139 ggatttccag aaggtattct cggagtagag ctcactgaca aattccgtaa acaatcggag 240
140 cgattcggta ctacgatatt tacagagacg gtgacgaaag tcgatttctc ttcgaaaccg 300
141 tttaagctat tcacagattc aaaagccatt ctcgctgacg ctgtgattct cgctatcgga 360
142 gctgtggcta agtggcttag cttcgttgga tctggtgaag ttctcggagg tttgtggaac 420
143 cgtggaatct ccgcttgtgc tgtttgcgac ggagctgctc cgatattccg caacaaacct 480
144 cttgcggtga tcggtggagg cgattctgca atggaagaag caaactttct tacaaaatat 540
145 ggatctaaag tgtatataat cgataggaga gatgctttta gagcgtctaa gattatgcag 600
146 cagcgagctt tgtctaatcc taagattgat gtgatttgga actcgtctgt tgtggaagct 660
147 tatggagatg gagaaagaga tgtgcttgga ggattgaaag tgaagaatgt ggttaccgga 720
148 gatgtttctg atttaaaagt ttctggattg ttctttgcta ttggtcatga gccagctacc 780
149 aagtttttgg atggtggtgt tgagttagat tcggatggtt atgttgtcac gaagcctggt 840
150 actacacaga ctagcgttcc cggagttttc gctgcgggtg atgttcagga taagaagtat 900
151 aggcaagcca tcactgctgc aggaactggg tgcatggcag ctttggatgc agagcattac 960
152 ttacaagaga ttggatctca gcaaggtaag agtgattga                         999
154 <210> SEQ ID NO: 10
155 <211> LENGTH: 1002
156 <212> TYPE: DNA
157 <213> ORGANISM: Artificial Sequence
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162 <221> NAME/KEY: CDS
163 <222> LOCATION: (1)...(1002)
164 <223> OTHER INFORMATION: cDNA encoding NADPH thioredoxin reductase
166 <400> SEQUENCE: 10
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169 1               5                   10                  15
171 ggc cca gcg gca cac acg gcg gcg att tac gca gct agg gct gaa ctt   96
172 Gly Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu
173             20                  25                  30
175 aaa cct ctt ctc ttc gaa gga tgg atg gct aac gac atc gct ccc ggt  144
176 Lys Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly
177         35                  40                  45
179 ggt caa cta aca acc acc acc gac gtc gag aat ttc ccc gga ttt cca  192
180 Gly Gln Leu Thr Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro
181     50                  55                  60
183 gaa ggt att ctc gga gta gag ctc act gac aaa ttc cgt aaa caa tcg  240
184 Glu Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser
185 65                  70                  75                  80
187 gag cga ttc ggt act acg ata ttt aca gag acg gtg acg aaa gtc gat  288
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188 Glu Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp
189                 85                  90                  95
191 ttc tct tcg aaa ccg ttt aag cta ttc aca gat tca aaa gcc att ctc     336
192 Phe Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu
193             100                 105                 110
195 gct gac gct gtg att ctc gct act gga gct gtg gct aag cgg ctt agc     384
196 Ala Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser
197             115                 120                 125
199 ttc gtt gga tct ggt gaa ggt tct gga ggt ttc tgg aac cgt gga atc     432
200 Phe Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile
201         130                 135                 140
203 tcc gct tgt gct gtt tgc gac gga gct gct ccg ata ttc cgt aac aaa     480
204 Ser Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys
205 145                 150                 155                 160
207 cct ctt gcg gtg atc ggt gga ggc gat tca gca atg gaa gaa gca aac     528
208 Pro Leu Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn
209             165                 170                 175
211 ttt ctt aca aaa tat gga tct aaa gtg tat ata atc cat agg aga gat     576
212 Phe Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp
213             180                 185                 190
215 gct ttt aga gcg tct aag att atg cag cag cga gct ttg tct aat cct     624
216 Ala Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro
217             195                 200                 205
219 aag att gat gtg att tgg aac tcg tct gtt gtg gaa gct tat gga gat     672
220 Lys Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp
221         210                 215                 220
223 gga gaa aga gat gtg ctt gga gga ttg aaa gtg aag aat gtg gtt acc     720
224 Gly Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr
225 225                 230                 235                 240
227 gga gat gtt tct gat tta aaa gtt tct gga ttg ttc ttt gct att ggt     768
228 Gly Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly
229             245                 250                 255
231 cat gag cca gct acc aag ttt ttg gat ggt ggt gtt gag tta gat tcg     816
232 His Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser
233             260                 265                 270
235 gat ggt tat gtt gtc acg aag cct gga act aca cag act agc gtt ccc     864
236 Asp Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro
237         275                 280                 285
239 gga gtt ttc gct gcg ggt gat gtt cag gat aag aag tat agg caa gcc     912
240 Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala
241         290                 295                 300
243 atc act gct gca gga act ggg tgc atg gca gct ttg gat gca gag cat     960
244 Ile Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His
245 305                 310                 315                 320
247 tac tta caa gag att gga tct cag caa ggt aag agt gat tga            1002
248 Tyr Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp  *
249             325                 330
253 <210> SEQ ID NO: 11
254 <211> LENGTH: 333
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RAW SEQUENCE LISTING   DATE: 01/15/2002
PATENT APPLICATION: US/10/032,201   TIME: 08:06:13

Input Set : A:\351bseq.001
Output Set: N:\CRF3\01152002\J032201.raw

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255 <212> TYPE: PRT
256 <213> ORGANISM: Artificial Sequence
258 <220> FEATURE:
259 <223> OTHER INFORMATION: Chimeric
261 <400> SEQUENCE: 11
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265             20                  25                  30
266 Lys Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly
267         35                  40                  45
268 Gly Gln Leu Thr Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro
269     50                  55                  60
270 Glu Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser
271 65                  70                  75                  80
272 Glu Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp
273             85                  90                  95
274 Phe Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu
275             100                 105                 110
276 Ala Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser
277         115                 120                 125
278 Phe Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile
279     130                 135                 140
280 Ser Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys
281 145                 150                 155                 160
282 Pro Leu Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn
283             165                 170                 175
284 Phe Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp
285         180                 185                 190
286 Ala Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro
287         195                 200                 205
288 Lys Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp
289     210                 215                 220
290 Gly Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr
291 225                 230                 235                 240
292 Gly Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly
293             245                 250                 255
294 His Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser
295         260                 265                 270
296 Asp Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro
297         275                 280                 285
298 Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala
299     290                 295                 300
300 Ile Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His
301 305                 310                 315                 320
302 Tyr Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp
303             325                 330
306 <210> SEQ ID NO: 12
307 <211> LENGTH: 332
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<210> 17
<211> 118
<212> PRT *Artificial*
<213> (Artifcial) sequence   *see item 11 on Error Summary Sheet*

<400> 17

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Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr
            35              40              45
Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu
    50              55              60
Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile
65              70              75              80
Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile
            85              90              95
Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val
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Phe Ser Trp Ile Tyr Lys
            115
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<210> 18
<211> 169
<212> PRT   *misspelled → please correct this spelling error globally*
<213> (Artifcial) sequence   *see item 11*

<400> 18

Input Set : **A:\351bseq.001**
Output Set: **N:\CRF3\01152002\J032201.raw**

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L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:533 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:678 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:680 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:680 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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L:856 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:4706 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:101
L:4708 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:101
L:4710 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:101
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L:4899 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:109
L:4901 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:109
L:4905 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:109
L:5488 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:134
L:5490 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:134
L:9691 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:245
L:11042 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:275
L:11599 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:287
L:11696 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:288
L:11849 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:290
L:12072 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:293
L:12159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:294
L:12238 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:295
L:12323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:296
L:12638 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:300
L:12851 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:303
L:12930 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:304
L:13153 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:307
L:13260 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:309
L:13419 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:312
L:13496 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:313